RAW SEQUENCE LISTING ERROR REPORT

BIC CHNOLOGY
SYSTEMS
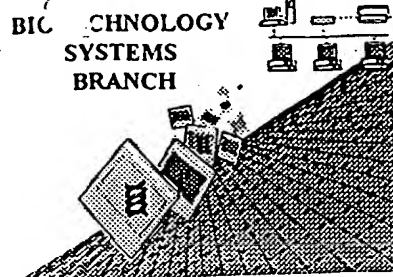BRANCH

#4

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/882,434_

Source: _OIPE_

Date Processed by STIC: _7/5/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY** or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be downloaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/882,434   TIME: 11:28:47

Input Set : A:\CULLNCP.txt
Output Set: N:\CRF3\07052001\I882434.raw

```
      4 <110> APPLICANT: Manners, John M.
      5         Marcus, John Paul
      6         Goulter, Kenneth C.
      7         Green, Jodie Lyn
      8         Harrison, Stuart John
     10 <120> TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
     12 <130> FILE REFERENCE: CULLN18.1CP1C1
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/882,434
C--> 14 <141> CURRENT FILING DATE: 2001-06-15
     14 <150> PRIOR APPLICATION NUMBER: 09/364395
     15 <151> PRIOR FILING DATE: 1999-07-30
     17 <150> PRIOR APPLICATION NUMBER: 09/117615
     18 <151> PRIOR FILING DATE: 1998-11-09
     20 <150> PRIOR APPLICATION NUMBER: PCT/AU97/00052
     21 <151> PRIOR FILING DATE: 1997-01-31
     23 <150> PRIOR APPLICATION NUMBER: AU PN 7802
     24 <151> PRIOR FILING DATE: 1996-01-31
     26 <160> NUMBER OF SEQ ID NOS: 21
     28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     30 <210> SEQ ID NO: 1
     31 <211> LENGTH: 102
     32 <212> TYPE: PRT
     33 <213> ORGANISM: Macadamia integrifolia
     35 <400> SEQUENCE: 1
     36 Met Ala Ser Thr Lys Leu Phe Phe Ser Val Ile Thr Val Met Met Leu
     37  1               5                   10                  15
     38 Ile Ala Met Ala Ser Glu Met Val Asn Gly Ser Ala Phe Thr Val Trp
     39              20                  25                  30
     40 Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu Arg Tyr Ser Lys Cys Gly
     41          35                  40                  45
     42 Cys Ser Ala Ile His Gln Lys Gly Gly Tyr Asp Phe Ser Tyr Thr Gly
     43      50                  55                  60
     44 Gln Thr Ala Ala Leu Tyr Asn Gln Ala Gly Cys Ser Gly Val Ala His
     45 65                  70                  75                  80
     46 Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys Asn Pro Phe Gly Trp Lys
     47              85                  90                  95
     48 Ser Ile Phe Ile Gln Cys
     49              100
     51 <210> SEQ ID NO: 2
     52 <211> LENGTH: 493
     53 <212> TYPE: DNA
     54 <213> ORGANISM: Macadamia integrifolia
     56 <220> FEATURE:
     57 <221> NAME/KEY: CDS
     58 <222> LOCATION: (70)...(375)
     59 <223> OTHER INFORMATION: y=t or c.
     61 <400> SEQUENCE: 2
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```
62 attaagtctt tgagtctcat acatactctt ctcctcccca ccattagcac ttatcagcta        60
63 acctcagcc atg gct tcc acc aag ttg ttc ttc tca gtc att act gtg atg       111
64           Met Ala Ser Thr Lys Leu Phe Phe Ser Val Ile Thr Val Met
65            1               5                  10
67 atg ctc ata gca atg gca agt gag atg gtg aat ggg agt gca ttt aca         159
68 Met Leu Ile Ala Met Ala Ser Glu Met Val Asn Gly Ser Ala Phe Thr
69  15                  20                  25                  30
71 gta tgg agt ggt cca ggt tgt aac aac cgt gct gag cga tat agc aag         207
72 Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu Arg Tyr Ser Lys
73                  35                  40                  45
75 tgt gga tgc tca gct ata cat cag aag gga ggc tat gac ttc agc tac         255
76 Cys Gly Cys Ser Ala Ile His Gln Lys Gly Gly Tyr Asp Phe Ser Tyr
77                  50                  55                  60
79 act gga caa act gct gct ctc tac aac cag gct gga tgc agt ggt gtt         303
80 Thr Gly Gln Thr Ala Ala Leu Tyr Asn Gln Ala Gly Cys Ser Gly Val
81          65                  70                  75
83 gca cac acc agg ttt ggg tcc agt gcc agg gca tgc aac cct ttt ggt         351
84 Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys Asn Pro Phe Gly
85       80                  85                  90
87 tgg aag agt atc ttc atc caa tgc tagatttcat aactcttgga tccatcttct        405
88 Trp Lys Ser Ile Phe Ile Gln Cys
89  95                 100
91 atgtttttca agtgtataat tagagagatg catggatata taataaataa gtaaaagcta       465
92 cggtatcacc atgtgatgat tttyaccc                                          493
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94 <210> SEQ ID NO: 3
95 <211> LENGTH: 19
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Degenerate primer alpha.
102 <400> SEQUENCE: 3
103 ccgaagcagt tgcabgcbc   19
105 <210> SEQ ID NO: 4
106 <211> LENGTH: 20
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Degenerate primer beta.
113 <400> SEQUENCE: 4
114 gagmgktatw skaagtgtgg   20
116 <210> SEQ ID NO: 5
117 <211> LENGTH: 20
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: 3' RACE primer alpha.
124 <400> SEQUENCE: 5
125 tgctctctac aaccaggctg   20
127 <210> SEQ ID NO: 6

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Input Set : A:\CULLNCP.txt
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```
128 <211> LENGTH: 19
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: 5' RACE primer beta.
135 <400> SEQUENCE: 6                                               19
136 gcattggatg aagatactc
138 <210> SEQ ID NO: 7
139 <211> LENGTH: 36
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: 5' RACE primer to anneal with poly-C-tailed cDNA
145       primer alpha.
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: (0)...(0)
149 <223> OTHER INFORMATION: n = inosine
151 <400> SEQUENCE: 7
152 ggccacgcgt cgactagtac gggnngggnn gggnng                        36
154 <210> SEQ ID NO: 8
155 <211> LENGTH: 20
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Mi28K primer. Mismatched oligonucleotide
161       containing a mutation of the MiAMP1 coding
162       sequence from amino acid Q(position 28) to K.
164 <400> SEQUENCE: 8                                               20
165 gctatacata aaaagggagg
167 <210> SEQ ID NO: 9
168 <211> LENGTH: 20
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Mi39K primer. Mismatched oligonucleotide
174       containing a mutation of the MiAMP1 coding
175       sequence from amino acid Q(position 39) to K.
177 <400> SEQUENCE: 9                                               20
178 tacactggaa aaactgctgc
180 <210> SEQ ID NO: 10
181 <211> LENGTH: 24
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Mi46K primer. Mismatched oligonucleotide
187       containing a mutation of the MiAMP1 coding
188       sequence from amino acid Q(position 46) to K.
190 <400> SEQUENCE: 10                                              24
191 gcatccagct ttgttgtaga gagc
```

[handwritten annotation] must give location of each "n" or a range that includes all "n's" present.

[handwritten marker at left of line 152] W-->

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PATENT APPLICATION: US/09/882,434   TIME: 11:28:47

Input Set : A:\CULLNCP.txt
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193 <210> SEQ ID NO: 11
194 <211> LENGTH: 24
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Mi54V primer. Mismatched oligonucleotide
200   containing a mutation of the MiAMP1 coding
201   sequence from amino acid H(position 54) to V.
203 <400> SEQUENCE: 11
204 ggtgttgcag tgaccaggtt tggg   24
206 <210> SEQ ID NO: 12
207 <211> LENGTH: 24
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Mi54K primer. Mismatched oligonucleotide
213   containing a mutation of the MiAMP1 coding
214   sequence from amino acid H(position 54) to K.
216 <400> SEQUENCE: 12
217 ggtgttgcaa aaaccaggtt tggg   24
219 <210> SEQ ID NO: 13
220 <211> LENGTH: 31
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Oligonucleotide primer from the 5' coding region
226   of MiAMP1 (Mi1 primer).
228 <400> SEQUENCE: 13
229 acaccatatg agtgcattta cagtatgagt g   31
231 <210> SEQ ID NO: 14
232 <211> LENGTH: 35
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Oligonucleotide primer from the 3' coding region
238   of MiAMP1 (Mi2 primer).
240 <400> SEQUENCE: 14
241 gaagagtatc ttcatccaat gctaaggatc cacac   35
243 <210> SEQ ID NO: 15
244 <211> LENGTH: 76
245 <212> TYPE: PRT
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Mi28K variant. Variant MiAMP1 protein Mi28K
250   containing a Lysine at amino acid 28 (used primer
251   from SEQ ID NO:8 to produce).
253 <400> SEQUENCE: 15
254 Ser Ala Phe Thr Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu
255 1   5   10   15

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```
256 Arg Tyr Ser Lys Cys Gly Cys Ser Ala Ile His Lys Lys Gly Gly Tyr
257              20              25              30
258 Asp Phe Ser Tyr Thr Gly Gln Thr Ala Ala Leu Tyr Asn Gln Ala Gly
259          35          ..    40              45
260 Cys Ser Gly Val Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys
261      50              55              60
262 Asn Pro Phe Gly Trp Lys Ser Ile Phe Ile Gln Cys
263 65              70              75
265 <210> SEQ ID NO: 16
266 <211> LENGTH: 76
267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Mi39K variant. Variant MiAMP1 protein Mi39K
272        containing a Lysine at amino acid 39 (used primer
273        from SEQ ID NO:9 to produce).
275 <400> SEQUENCE: 16
276 Ser Ala Phe Thr Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu
277 1               5               10              15
278 Arg Tyr Ser Lys Cys Gly Cys Ser Ala Ile His Gln Lys Gly Gly Tyr
279              20              25              30
280 Asp Phe Ser Tyr Thr Gly Lys Thr Ala Ala Leu Tyr Asn Gln Ala Gly
281          35              40              45
282 Cys Ser Gly Val Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys
283      50              55              60
284 Asn Pro Phe Gly Trp Lys Ser Ile Phe Ile Gln Cys
285 65              70              75
287 <210> SEQ ID NO: 17
288 <211> LENGTH: 76
289 <212> TYPE: PRT
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Mi46K variant. Variant MiAMP1 protein Mi46K
294        containing a Lysine at amino acid 46 (used primer
295.       from SEQ ID NO:10 to produce).
297 <400> SEQUENCE: 17
298 Ser Ala Phe Thr Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu
299 1               5               10              15
300 Arg Tyr Ser Lys Cys Gly Cys Ser Ala Ile His Gln Lys Gly Gly Tyr
301              20              25              30
302 Asp Phe Ser Tyr Thr Gly Gln Thr Ala Ala Leu Tyr Asn Lys Ala Gly
303          35              40              45
304 Cys Ser Gly Val Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys
305      50              55              60
306 Asn Pro Phe Gly Trp Lys Ser Ile Phe Ile Gln Cys
307 65              70              75
309 <210> SEQ ID NO: 18
310 <211> LENGTH: 76
311 <212> TYPE: PRT
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/882,434

DATE: 07/05/2001
TIME: 11:28:48

Input Set : A:\CULLNCP.txt
Output Set: N:\CRF3\07052001\I882434.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7